

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Roger  
Au-Young, Janice  
Bandman, Olga  
Seilhamer, Jeffrey J.
- (ii) TITLE OF INVENTION: C5a-Like Seven Transmembrane Receptor
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
  - (B) STREET: 3330 Hillview Avenue
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Luther, Barbara J.
  - (B) REGISTRATION NUMBER: 33954
  - (C) REFERENCE/DOCKET NUMBER: PF-0040 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1446 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: Mast Cell
  - (B) CLONE: 8118
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGTCTT	TCTCTGCTGA	GACCAATTCA	ACTGACCTAC	TCTCACAGCC	ATGGAATGAG	60
CCCCCAGTAA	TTCTCTCCAT	GGTCATTCTC	AGCCTTACTT	TTTTACTGGG	ATTGCCAGGC	120
AATGGGCTGG	TGCTGTGGGT	GGCTGGCCTG	AAGATGCAGC	GGACAGTGAA	CACAATTGG	180
TTCCCTCCACC	TCACCTTGGC	GGACCTCCTC	TGCTGCCCT	CCTTGGCCTT	CTCGCTGGCT	240
CACTTGGCTC	TCCAGGGACA	GTGGCCCTAC	GGCAGGTTCC	TATGCAAGCT	CATCCCCTCC	300
ATCATTGTCC	TCAACATGTT	TGGCAGTGTC	TTCCTGCTTA	CTGCCATTAG	CCTGGATCGC	360
TGTCTTGTGG	TATTCAAGCC	AATCTGGTGT	CAGAACATC	GCAATGTAGG	GATGGCCTGC	420
TCTATCTGTG	GATGTATCTG	GGTGGTGGCT	TTTGTGTTGT	GCATTCTGT	GTTCGTGTAC	480
CGGGAAATCT	TCACTACAGA	CAACCATAAT	AGATGTGGCT	ACAAATTGG	TCTCTCCAGC	540
TCATTAGATT	ATCCAGACTT	TTATGGGGAT	CCACTAGAAA	ACAGGTCTCT	TGAAAACATT	600
GTTCAGCCGC	CTGGAGAAAT	GAATGATAGG	TTAGATCCTT	CCTCTTCCA	AACAAATGAT	660
CATCCTTGGG	CAGTCCCCAC	TGTCTTCCAA	CCTCAAACAT	TTCAAAGACC	TTCTGCAGAT	720
TCACTCCCTA	GGGGTTCTGC	TAGGTTAACCA	AGTAAAATC	TGTATTCTAA	TGTATTTAAA	780
CCTGCTGATG	TGGTCTCACC	TAAAATCCCC	AGTGGGTTTC	CTATTGAAGA	TCACGAAACC	840
AGCCCACGG	ATAACTCTGA	TGCTTTCTC	TCTACTCATT	TAAAGCTGTT	CCCTAGCGCT	900
TCTAGCAATT	CCTTCTACGA	GTCTGAGCTA	CCACAAGGTT	TCCAGGATTA	TTACAATTAA	960
GGCCAATTCA	CAGATGACGA	TCAAGTGCCA	ACACCCCTCG	TGGCAATAAC	GATCACTAGG	1020
CTAGTGGTGG	GTTCCTGCT	GCCCTCTGTT	ATCATGATAG	CCTGTTACAG	CTTCATTGTC	1080
TTCCGAATGC	AAAGGGGCCG	CTTCGCCAAG	TCTCAGAGCA	AAACCTTCG	AGTGGCCGTG	1140
GTGGTGGTGG	CTGTCTTCT	TGTCTGCTGG	ACTCCATACC	ACATTGGGG	AGTCCTGTCA	1200
TTGCTTACTG	ACCCAGAAC	TCCCTGGGG	AAAACCTCTGA	TGTCTGGGA	TCATGTATGC	1260
ATTGCTCTAG	CATCTGCCAA	TAGTTGCTTT	AATCCCTTCC	TTTATGCCCT	CTTGGGGAAA	1320
GATTTTAGGA	AGAAAGCAAG	GCAGTCCATT	CAGGAAATTC	TGGAGGCAGC	CTTCAGTGAG	1380
GAGCTCACAC	GTTCCACCCA	CTGTCCCTCA	AACAATGTCA	TTTCAGAAAG	AAATAGTACA	1440
ACTGTG						1446

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 482 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Phe Ser Ala Glu Thr Asn Ser Thr Asp Leu Leu Ser Gln  
1 5 10 15

Pro Trp Asn Glu Pro Pro Val Ile Leu Ser Met Val Ile Leu Ser Leu  
20 25 30

Thr Phe Leu Leu Gly Leu Pro Gly Asn Gly Leu Val Leu Trp Val Ala  
35 40 45

Gly Leu Lys Met Gln Arg Thr Val Asn Thr Ile Trp Phe Leu His Leu  
50 55 60

Thr Leu Ala Asp Leu Leu Cys Cys Leu Ser Leu Ala Phe Ser Leu Ala  
65 70 75 80

His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys  
85 90 95

Leu Ile Pro Ser Ile Ile Val Leu Asn Met Phe Gly Ser Val Phe Leu  
100 105 110

Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Val Val Phe Lys Pro Ile  
115 120 125

Trp Cys Gln Asn His Arg Asn Val Gly Met Ala Cys Ser Ile Cys Gly  
130 135 140

Cys Ile Trp Val Val Ala Phe Val Leu Cys Ile Pro Val Phe Val Tyr  
145 150 155 160

Arg Glu Ile Phe Thr Thr Asp Asn His Asn Arg Cys Gly Tyr Lys Phe  
165 170 175

Gly Leu Ser Ser Ser Leu Asp Tyr Pro Asp Phe Tyr Gly Asp Pro Leu  
180 185 190

Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn  
195 200 205

Asp Arg Leu Asp Pro Ser Ser Phe Gln Thr Asn Asp His Pro Trp Thr  
210 215 220

Val Pro Thr Val Phe Gln Pro Gln Thr Phe Gln Arg Pro Ser Ala Asp  
225 230 235 240

Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser  
245 250 255

Asn Val Phe Lys Pro Ala Asp Val Val Ser Pro Lys Ile Pro Ser Gly  
260 265 270

Phe Pro Ile Glu Asp His Glu Thr Ser Pro Leu Asp Asn Ser Asp Ala  
275 280 285

Phe Leu Ser Thr His Leu Lys Leu Phe Pro Ser Ala Ser Ser Asn Ser  
290 295 300

Phe Tyr Glu Ser Glu Leu Pro Gln Gly Phe Gln Asp Tyr Tyr Asn Leu  
305 310 315 320

Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile  
325 330 335

Thr Ile Thr Arg Leu Val Val Gly Phe Leu Leu Pro Ser Val Ile Met  
340 345 350

Ile Ala Cys Tyr Ser Phe Ile Val Phe Arg Met Gln Arg Gly Arg Phe  
355 360 365

Ala Lys Ser Gln Ser Lys Thr Phe Arg Val Ala Val Val Val Ala  
370 375 380

Val Phe Leu Val Cys Trp Thr Pro Tyr His Ile Trp Gly Val Leu Ser  
385 390 395 400

Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp  
405 410 415

Asp His Val Cys Ile Ala Leu Ala Ser Ala Asn Ser Cys Phe Asn Pro  
420 425 430

Phe Leu Tyr Ala Leu Leu Gly Lys Asp Phe Arg Lys Lys Ala Arg Gln  
435 440 445

Ser Ile Gln Gly Ile Leu Glu Ala Ala Phe Ser Glu Glu Leu Thr Arg  
450 455 460

Ser Thr His Cys Pro Ser Asn Asn Val Ile Ser Glu Arg Asn Ser Thr  
465 470 475 480

Thr Val